

Cyr61	M--SSSTFRTLAVAVTLIHL--TRIALST-CPAAC--HGFLE-APKCAPGVGLVLDGGRGKGRK	58
CEf10	M--GSAGARP-ALAAAILCL--ARLALGSPCPAVC--QGFPA-ABQCAPGVGLVLDGGRGKGRK	58
Fisp12	M--LASVAGTISLA-LVLLALCTRPATGQDCSAQC--QCAAEAPFPCAGVSLVLDGGRGKGRK	61
CTGF	M--TAASHGTVRVAFVVLALCSRPAVQONCSGPC--RCTDEPAPFPCAGVSLVLDGGRGKGRK	62
Nov	METGGGGLFVLLIIIIILRPFCEVSGREAACPRCGGRCPAEP-PRCAPGVPAVLDDGGGGLNGAR	65
Cyr61	QLNEDCSKTQPCDHTKGLECNFGASSTALNGICRAQSEGRFCEYNSTKYONGESTQPNCKHQCTCI	124
CEf10	QLNEDCSKTQPCDHTKGLECNFGASPAATNGICRAQSEGRFCEYNSTKYONGESTQPNCKHQCTCI	124
Fisp12	QLGZLCTERDECDPHKGLFCDFGSPANRKGIVCTAK-DGAPCVFGGSVYRSSESSTQSNKYQCTCI	126
CTGF	QLGZLCTERDECDPHKGLFCDFGSPANRKGIVCTAK-DGAPCVFGGSVYRSSESSTQSNKYQCTCI	127
Nov	QRGZCSFLLPCDESGETYCDRGPEDGGGAGLQNVL-EGDNQVFDGKIDRNGETEDPSLKYQCTCI	130
Cyr61	DGAVGCTFLCPQELSTPNLGGFNPRLVKVSGCCGEFVCDSDSIK-DSLDD-QDDLLGLDASEVL	188
CEf10	DGAVGCTFLCPQELSTPNLGGFNPRLVKVSGCCGEFVCDSDSDALEELEGFFSKFGLDASEGL	190
Fisp12	DGAVGCVFLCSHVRPLSPDCPFPRRVKLPCKCCGEFVCDSEPKDKTAVGP-----ALAKYRLSD	185
CTGF	DGAVGCVFLCSHVRPLSPDCPFPRRVKLPCKCCGEFVCDSEPKDKTAVGP-----ALAKYRLSD	186
Nov	DGQIGGLFPCNLGLLLPCPDGPFPRKI EVPGCCCKVCDPRDEVLLGCT-----ANAKYRQEA	189
Cyr61	TRNNELIAIGKSSSLQKLPVTCTEPRVLFNPLHANGQKCTVQTTSSQCSKSGGTGLSTKVTNDMP	254
CEf10	TRNNELIAIVKGG-LQMLPVTCSEPO-----SRAFENPKCTVQTTSSQCSKSGGTGLSTKVTNDMP	251
Fisp12	T-----FGPDF-----THIRANGLVQTTSSQCSKSGGTGLSTKVTNDMP	225
CTGF	T-----FGPDF-----THIRANGLVQTTSSQCSKSGGTGLSTKVTNDMP	226
Nov	T-----LGIDV-----SDSSANGTEQTTSSQCSKSGGTGLSTKVTNDMP	229
Cyr61	ECRLVKETRIEVRPCGQPVYSSLIQKGRKSKTKKSPEPVRFYAGCSSVQGRPKYCGSVDGRG	320
CEf10	DCKLIKETRIEVRPCGQPSYASLIQKGRKSKTKKSPEPVRFYAGCSSVQGRPKYCGSVDGRG	317
Fisp12	FCRLKQSELRVRECEADLEENIKGGRKCTRTPKLAKPVKFLSGGTSVQTYRAKFGGVTGGRG	291
CTGF	SCRLEKQSELRVRECEADLEENIKGGRKCTRTPKLAKPVKFLSGGTSVQTYRAKFGGVTGGRG	292
Nov	QCEVKEQTELRVRECEADLEENIKGGRKCTRTPKLAKPVKFLSGGTSVQTYRAKFGGVTGGRG	294
Cyr61	CTPLOTRTVQKFRCDGEDGFTSIVVM-IQSCRCNYNCPHREASTRLY--SLFNDIHKFRD	379
CEf10	CTPQOTRTVQKFRCDGEDGFTTKSVVM-IQSCRCNYNCPHANEAYFFY--RLVNDIHKFRD	376
Fisp12	CTPHRTTTLFVEFKCPDGEIQQON-HMFIKTCACHYNCPCDNDIFESLYRYMYGDMA	348
CTGF	CTPHRTTTLFVEFKCPDGEIQQON-HMFIKTCACHYNCPCDNDIFESLYRYMYGDMA	349
Nov	CTPHNDKTIQVEFRCPQGGFLKKP-HMLNTGVCHGNCPCSKNAFTQPLDPMSSSEAKI	351

FIGURE 1

M--SSSTFRTLAVAVTLLHL--TRLALST-CPAAC--HCPL-APKCAPGVGLVRDGGCGCKVCAK 58  
 M--GSAGARP-ALAAALLCL--ARLALGSPCPAVC--QCPAA-APQCAPGVGLVPDGGCGCKVCAK 58  
 M--LASVAGPISLA-LVLLALCTRPATGQDCSAQC--OCAAEEAAPHCPAGVSLVLDGGCGCCRCAK 61  
 M--TAASMGVVRVAFVLLALCSRPAVGQNCSGPC--RCPDEPAPRPCAGVSLVLDGGCGCCRCAK 62  
 METGGGQGLPVLLLLLLLRPCEVSGREAAACPRCGGRCPAEP-PRCAPGVPAVLDDGGCGCCLVCAR 65  
 CYR61  
 CEF10  
 FISP12  
 CTGF  
 NOV

QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCYNSRIYONGESFOPNCKHQCTCI 124  
 QLNEDCSRTQPCDHTKGLECNFGASPAATNGICRAQSEGRPCYNSKIYONGESFOPNCKHQCTCI 124  
 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFOSCKYQCTCL 126  
 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCIFGGTVYRSGESFOSCKYQCTCL 127  
 ORGESCSPLPCDESGLYCDRGPEDGGGAGICMVL-EGDNCVFDGMIYRNGETFOPSCKYQCTCR 130  
 CYR61  
 CEF10  
 FISP12  
 CTGF  
 NOV

DGAVGCIPLCQELSLPNLGCNPRLVKVSQCCEEWVCEDESIK-DSLDD-ODDLLGLDASEVEL 188  
 DGAVGCIPLCQELSLPNLGCNPSRPLVKVPGQCCEEWVCEDESKDALEEELEGGFSKEFGLDASEGEL 190  
 DGAVGCVPLCSMDVRLSPDCPFPRRVKLPKGCKCKEWVCEDEPKDRTAVGP-----ALAAAYRLED 185  
 DGAVGCMPLCSMDVRLSPDCPFPRRVKLPKGCKCEEWVCEDEPKDQTVVGP-----ALAAAYRLED 186  
 DGQIGCLPRCNLGLLLPGPDCPFPRKIEVPGECKEWVCDPRDEVLLGGF-----AMAAAYRQEA 189  
 CYR61  
 CEF10  
 FISP12  
 CTGF  
 NOV

FIGURE 1 (1 of 2)

Cyr61	TRNNELIAIGKSSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTWSQCSKSGTGISTRVTNDNP	254
CEF10	TRNNELIAIVKGG-LKMLPVFGSEPQ-----SRAFENPKCIVQTTWSQCSKTCGTGISTRVTNDNP	251
Fisp12	T-----FGPDP-----TMMRANCLVQTTESACSKTCGMGISTRVTNDNT	225
CTGF	T-----FGPDP-----TMIRANCLVQTTESACSKTCGMGISTRVTNDNA	226
Nov	T-----LGIDV-----SDSSANCIEQTTESACSKSCGMGFSTRVTRNQ	229

Cyr61	ECRLVKETRICEVRPCGQPVYSSLKGGKKCKTKKSPPEVRFTYAGCSSVKKYRPKYCGSCVDGRC	320
CEF10	DCKLIKETRICEVRPCGQPSYASLKGKKCTKTKSPSPVRFTYAGCSSVKKYRPKYCGSCVDGRC	317
Fisp12	FCRLEKOSRLCMVRPCEADLEENIKGKKCIRTPIAKPVKFELSGCTSVKTYRAKFCGVCTDGRC	291
CTGF	SCRLEKOSRLCMVRPCEADLEENIKGKKCIRTPIKSKPIKFELSGCTSMKTYRAKFCGVCTDGRC	292
Nov	QCEMVKQTRLCMMRPCEN-EEPSDKGKKCIOTKSKMAVRFEYKNCTSVQTYKPRYCGLCNDGRC	294

Cyr61	CTPLQTRTVKMRFCEDGEMFSKNVMM-IQSCCKNYNCPHPNEASFRLY--SLFNDIHKFRD	379
CEF10	CTPQQTRTVKIRFRCDGGETFTKSVM-IOSCRCNYNCPHANE-YPFY--RLVNDIHKFRD	376
Fisp12	CTPHRTTTLPVEFKCPDGEIMKKN-MMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	348
CTGF	CTPHRTTTLPVEFKCPDGEVMKKN-MMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	349
Nov	CTPHNTKTIQVEFRCPQGKFLKPP-MMLINTCVCHGNCPOSNAFFQPLDPMSEAKI	351

FIGURE 1 (2 of 2)